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SEQUENCE LISTING

<110> The Scripps Research Institute  
The Regents of the University of California  
Wu, Eugene  
Nemerow, Glen R.  
Stewart, Phoebe

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&lt;223&gt; primer

&lt;400&gt; 26

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-18-

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Asp	Ile	Asn	Pro	Ile	Lys	Thr	Lys	Ile	Gly	Ser	Gly	Ile	Asp	Tyr	Asn
						355			360			365			
Glu	Asn	Gly	Ala	Met	Ile	Thr	Lys	Leu	Gly	Ala	Gly	Leu	Ser	Phe	Asp
						370			375			380			
Asn	Ser	Gly	Ala	Ile	Thr	Ile	Gly	Asn	Lys	Asn	Asp	Asp	Lys	Leu	Thr
						385			390			395			400
Leu	Trp	Thr	Thr	Pro	Asp	Pro	Ser	Pro	Asn	Cys	Arg	Ile	His	Ser	Asp
						405			410			415			
Asn	Asp	Cys	Lys	Phe	Thr	Leu	Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Val
						420			425			430			
Leu	Ala	Thr	Val	Ala	Ala	Leu	Ala	Val	Ser	Gly	Asp	Leu	Ser	Ser	Met
						435			440			445			
Thr	Gly	Thr	Val	Ala	Ser	Val	Ser	Ile	Phe	Leu	Arg	Phe	Asp	Gln	Asn
						450			455			460			
Gly	Val	Leu	Met	Glu	Asn	Ser	Ser	Leu	Lys	Lys	His	Tyr	Trp	Asn	Phe
						465			470			475			480
Arg	Asn	Gly	Asn	Ser	Thr	Asn	Ala	Asn	Pro	Tyr	Thr	Asn	Ala	Val	Gly
						485			490			495			
Phe	Met	Pro	Asn	Leu	Leu	Ala	Tyr	Pro	Lys	Thr	Gln	Ser	Gln	Thr	Ala
						500			505			510			
Lys	Asn	Asn	Ile	Val	Ser	Gln	Val	Tyr	Leu	His	Gly	Asp	Lys	Thr	Lys
						515			520			525			
Pro	Met	Ile	Leu	Thr	Ile	Thr	Leu	Asn	Gly	Thr	Ser	Glu	Ser	Thr	Glu
						530			535			540			
Thr	Ser	Glu	Val	Ser	Thr	Tyr	Ser	Met	Ser	Phe	Thr	Trp	Ser	Trp	Glu
						545			550			555			560
Ser	Gly	Lys	Tyr	Thr	Thr	Glu	Thr	Phe	Ala	Thr	Asn	Ser	Tyr	Thr	Phe
						565			570			575			
Ser	Tyr	Ile	Ala	Gln	Glu										
					580										

<210> 34  
<211> 1746  
<212> DNA  
<213> Adenovirus serotype 5 fiber

<220>  
<221> CDS  
<222> (1)...(1746)

<400> 34

-19-

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro 1 5 10 15	48
tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro 20 25 30	96
ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser 35 40 45	144
ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu 50 55 60	192
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser 65 70 75 80	240
caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac Gln Asn Val Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn 85 90 95	288
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu 100 105 110	336
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr 115 120 125	384
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile 130 135 140	432
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln 145 150 155 160	480
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr 165 170 175	528
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu 180 185 190	576
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly 195 200 205	624
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr 210 215 220	672
ggc cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr 225 230 235 240	720
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca	768

-20-

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala			
245	250	255	
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt		816	
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val			
260	265	270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag		864	
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln			
275	280	285	
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac		912	
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn			
290	295	300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag		960	
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu			
305	310	315	320
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata		1008	
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile			
325	330	335	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca		1056	
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro			
340	345	350	
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat		1104	
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp			
355	360	365	
tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac		1152	
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp			
370	375	380	
agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act		1200	
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr			
385	390	395	400
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag		1248	
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu			
405	410	415	
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata		1296	
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile			
420	425	430	
ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata		1344	
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile			
435	440	445	
tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat		1392	
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn			
450	455	460	
gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt		1440	
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe			
465	470	475	480
aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga		1488	
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly			

-21-

485	490	495	
ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala 500	505		1536
aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys 515	520	510	1584
cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp 530	535	540	1632
aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly 545	550	555	1680
cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser 565	570	575	1728
tac att gcc caa gaa taa Tyr Ile Ala Gln Glu *			1746
	580		

<210> 35

<211> 581

<212> PRT

<213> Adenovirus serotype 5 fiber

<400> 35

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro	1	5	10	15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro	20	25	30	
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser	35	40	45	
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu	50	55	60	
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser	65	70	75	80
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn	85	90	95	
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu	100	105	110	
Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr	115	120	125	
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile	130	135	140	
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln	145	150	155	160
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr	165	170	175	
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu	180	185	190	
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly	195	200	205	
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr	210	215	220	

-22-

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
 225 230 235 240  
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
 245 250 255  
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
 260 265 270  
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
 275 280 285  
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
 290 295 300  
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
 305 310 315 320  
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
 325 330 335  
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
 340 345 350  
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
 355 360 365  
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
 370 375 380  
 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr  
 385 390 395 400  
 Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu  
 405 410 415  
 Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile  
 420 425 430  
 Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile  
 435 440 445  
 Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn  
 450 455 460  
 Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe  
 465 470 475 480  
 Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly  
 485 490 495  
 Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala  
 500 505 510  
 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys  
 515 520 525  
 Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp  
 530 535 540  
 Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly  
 545 550 555 560  
 His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser  
 565 570 575  
 Tyr Ile Ala Gln Glu  
 580

<210> 36  
 <211> 1098  
 <212> DNA  
 <213> Adenovirus serotype 37 fiber

<220>  
 <221> CDS  
 <222> (1)...(1098)

<400> 36  
 atg tca aag agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc 48  
 Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro  
 1 5 10 15

-23-

tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe 20 25 30	96
gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg gta ctg tca ctc Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu 35 40 45	144
aaa ctg gct gat cca atc acc att acc aat ggg gat gta tcc ctc aag Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys 50 55 60	192
gtg gga ggt ggt ctc act ttg caa gat gga agc cta act gta aac cct Val Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro 65 70 75 80	240
aag gct cca ctg caa gtt aat act gat aaa aaa ctt gag ctt gca tat Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr 85 90 95	288
gat aat cca ttt gaa agt agt gct aat aaa ctt agt tta aaa gta gga Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly 100 105 110	336
cat gga tta aaa gta tta gat gaa aaa agt gct gcg ggg tta aaa gat His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp 115 120 125	384
tta att ggc aaa ctt gtg gtt tta aca gga aaa gga ata ggc act gaa Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu 130 135 140	432
aat tta gaa aat aca gat ggt agc agc aga gga att ggt ata aat gta Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val 145 150 155 160	480
aga gca aga gaa ggg ttg aca ttt gac aat gat gga tac ttg gta gca Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala 165 170 175	528
tgg aac cca aag tat gac acg cgc aca ctt tgg aca aca cca gac aca Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr 180 185 190	576
tct cca aac tgc aca att gct caa gat aag gac tct aaa ctc act ttg Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu 195 200 205	624
gta ctt aca aag tgt gga agt caa ata tta gct aat gtg tct ttg att Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile 210 215 220	672
gtg gtc gca gga aag tac cac atc ata aat aat aag aca aat cca aaa Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Lys 225 230 235 240	720
ata aaa agt ttt act att aaa ctg cta ttt aat aag aac gga gtg ctt Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu 245 250 255	768

-24-

tta gac aac tca aat ctt gga aaa gct tat tgg aac ttt aga agt gga	816
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly	
260 265 270	
aat tcc aat gtt tcg aca gct tat gaa aaa gca att ggt ttt atg cct	864
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro	
275 280 285	
aat ttg gta gcg tat cca aaa ccc agt aat tct aaa aaa tat gca aga	912
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg	
290 295 300	
gac ata gtt tat gga act ata tat ctt ggt gga aaa cct gat cag cca	960
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro	
305 310 315 320	
gca gtc att aaa act acc ttt aac caa gaa act gga tgt gaa tac tct	1008
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser	
325 330 335	
atc aca ttt aac ttt agt tgg tcc aaa acc tat gaa aat gtt gaa ttt	1056
Ile Thr Phe Asn Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe	
340 345 350	
gaa acc acc tct ttt acc ttc tcc tat att gcc caa gaa tga	1098
Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu *	
355 360 365	

<210> 37

<211> 365

<212> PRT

<213> Adenovirus serotype 37 fiber

<400> 37

Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro	
1 5 10 15	
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe	
20 25 30	
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu	
35 40 45	
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys	
50 55 60	
Val Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro	
65 70 75 80	
Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr	
85 90 95	
Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly	
100 105 110	
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp	
115 120 125	
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu	
130 135 140	
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val	
145 150 155 160	
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala	
165 170 175	
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr	
180 185 190	
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu	

-25-

Val	Leu	Thr	Lys	Cys	Gly	Ser	195	200	205						
210						Gln	Ile	Leu	Ala	Asn	Val	Ser	Leu	Ile	
Val	Val	Ala	Gly	Lys	Tyr	His	215	215	220						
225						Ile	Ile	Asn	Asn	Lys	Thr	Asn	Pro	Lys	
Ile	Lys	Ser	Phe	Thr	Ile	Lys	Leu	Leu	Phe	Asn	Lys	Asn	Gly	Val	Leu
245						245	250	255							
Leu	Asp	Asn	Ser	Asn	Leu	Gly	Lys	Ala	Tyr	Trp	Asn	Phe	Arg	Ser	Gly
260						260	265	270							
Asn	Ser	Asn	Val	Ser	Thr	Ala	Tyr	Glu	Lys	Ala	Ile	Gly	Phe	Met	Pro
275						275	280	285							
Asn	Leu	Val	Ala	Tyr	Pro	Lys	Pro	Ser	Asn	Ser	Lys	Lys	Tyr	Ala	Arg
290						290	295	300							
Asp	Ile	Val	Tyr	Gly	Thr	Ile	Tyr	Leu	Gly	Gly	Lys	Pro	Asp	Gln	Pro
305						305	310	315							
Ala	Val	Ile	Lys	Thr	Thr	Phe	Asn	Gln	Glu	Thr	Gly	Cys	Glu	Tyr	Ser
325						325	330	335							
Ile	Thr	Phe	Asn	Phe	Ser	Trp	Ser	Lys	Thr	Tyr	Glu	Asn	Val	Glu	Phe
340						340	345	350							
Glu	Thr	Thr	Ser	Phe	Thr	Phe	Ser	Tyr	Ile	Ala	Gln	Glu			
355						355	360	365							

&lt;210&gt; 38

&lt;211&gt; 1098

&lt;212&gt; DNA

&lt;213&gt; Adenovirus serotype 19p fiber

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1098)

&lt;400&gt; 38

atg	tca	aag	agg	ctc	cgg	gtg	gaa	gat	gac	ttc	aac	ccc	gtc	tac	ccc
Met	Ser	Lys	Arg	Ieu	Arg	Val	Glu	Asp	Asp	Phe	Asn	Pro	Val	Tyr	Pro
1							5			10				15	

tat	ggc	tac	gcg	cgg	aat	cag	aat	atc	ccc	ttc	ctc	act	ccc	ccc	ttt
Tyr	Gly	Tyr	Ala	Arg	Asn	Gln	Asn	Ile	Pro	Phe	Leu	Thr	Pro	Pro	Phe
							20			25			30		

gtc	tcc	tcc	gat	gga	ttc	aaa	aac	ttc	ccc	cct	ggg	gta	ctg	tca	ctc
Val	Ser	Ser	Asp	Gly	Phe	Lys	Asn	Phe	Pro	Pro	Gly	Val	Leu	Ser	Leu
							35			40			45		

aaa	ctg	gct	gat	cca	atc	acc	att	acc	aat	ggg	gat	gta	tcc	ctc	aag
Lys	Leu	Ala	Asp	Pro	Ile	Thr	Ile	Thr	Asn	Gly	Asp	Val	Ser	Leu	Lys
							50			55			60		

gtg	gga	ggt	ggt	ctc	act	ttg	caa	gat	gga	agc	cta	act	gta	aac	cct
Val	Gly	Gly	Gly	Leu	Thr	Leu	Gln	Asp	Gly	Ser	Leu	Thr	Val	Asn	Pro
							65			70			75		80

aag	gct	cca	ctg	caa	gtt	act	act	gat	aaa	aaa	ctt	gag	ctt	gca	tat
Lys	Ala	Pro	Leu	Gln	Val	Thr	Thr	Asp	Lys	Lys	Leu	Glu	Leu	Ala	Tyr
							85			90			95		

gat	aat	cca	ttt	gaa	tgt	agt	gct	aat	aaa	ttt	agt	tta	aaa	gta	gga
Asp	Asn	Pro	Phe	Glu	Cys	Ser	Ala	Asn	Lys	Phe	Ser	Leu	Lys	Val	Gly
							100			105			110		

-26-

cat gga tta aaa gta tta gat gaa aaa agt gct gcg ggg tta aaa gat		384
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp		
115 120 125		
tta att ggc aaa ctt gtg gtt tta aca gga aaa gga ata ggc act gaa		432
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu		
130 135 140		
aat tta gaa aat aca gat ggt agc agc aga gga att ggt ata aat gta		480
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val		
145 150 155 160		
aga gca aga gaa ggg ttg aca ttt gac aat gat gga tac ttg gta gca		528
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala		
165 170 175		
tgg aac cca aag tat gac acg cgc aca ctt tgg aca aca cca gac aca		576
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Pro Asp Thr		
180 185 190		
tct cca aac tgc aca att gct cag gat aag gac tct aaa ctc act ttg		624
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu		
195 200 205 210		
gta ctt aca aag tgt gga agt caa ata tta gct aat gtg tct ttg att		672
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile		
210 215 220		
gtg gtc gca gga aag tac cac atc ata aat aat aag aca aat cca gaa		720
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Glu		
225 230 235 240		
ata aaa agt ttt act att aaa ctg tta ttt aat aag aac gga gtg ctt		768
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu		
245 250 255		
tta gac aac tca aat ctt gga aaa gct tat tgg aac ttt aga agt gga		816
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly		
260 265 270		
aat tcc aat gtt tcg aca gct tat gaa aaa gca att ggt ttt atg cct		864
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro		
275 280 285		
aat tta gta gcg tat cca aaa ccc agt aat tct aaa aaa tat gca aga		912
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg		
290 295 300		
gac ata gtt tat gga act ata tat ctt ggt gga aaa cct gat cag cca		960
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro		
305 310 315 320		
gca gtc att aaa act acc ttt aac caa gaa act gga tgt gaa tac tct		1008
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser		
325 330 335		
atc aca ttt gac ttt agt tgg tcc aaa acc tat gaa aat gtt gaa ttt		1056
Ile Thr Phe Asp Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe		
340 345 350		
gaa acc acc tct ttt acc ttc tcc tat att gcc caa gaa tga		1098

-27-

Glu	Thr	Thr	Ser	Phe	Thr	Phe	Ser	Tyr	Ile	Ala	Gln	Glu	*
355													
							360						
												365	

<210> 39  
<211> 365  
<212> PRT  
<213> Adenovirus serotype 19p fiber

<400> 39															
Met	Ser	Lys	Arg	Leu	Arg	Val	Glu	Asp	Asp	Phe	Asn	Pro	Val	Tyr	Pro
1							5			10				15	
Tyr	Gly	Tyr	Ala	Arg	Asn	Gln	Asn	Ile	Pro	Phe	Leu	Thr	Pro	Pro	Phe
20							25			30					
Val	Ser	Ser	Asp	Gly	Phe	Lys	Asn	Phe	Pro	Pro	Gly	Val	Leu	Ser	Leu
35							40					45			
Lys	Leu	Ala	Asp	Pro	Ile	Thr	Ile	Thr	Asn	Gly	Asp	Val	Ser	Leu	Lys
50							55			60					
Val	Gly	Gly	Leu	Thr	Leu	Gln	Asp	Gly	Ser	Leu	Thr	Val	Asn	Pro	
65							70			75				80	
Lys	Ala	Pro	Leu	Gln	Val	Thr	Thr	Asp	Lys	Lys	Leu	Glu	Leu	Ala	Tyr
85							90					95			
Asp	Asn	Pro	Phe	Glu	Cys	Ser	Ala	Asn	Lys	Phe	Ser	Leu	Lys	Val	Gly
100							105					110			
His	Gly	Leu	Lys	Val	Leu	Asp	Glu	Lys	Ser	Ala	Ala	Gly	Leu	Lys	Asp
115							120			125					
Leu	Ile	Gly	Lys	Leu	Val	Val	Leu	Thr	Gly	Lys	Gly	Ile	Gly	Thr	Glu
130							135			140					
Asn	Leu	Glu	Asn	Thr	Asp	Gly	Ser	Ser	Arg	Gly	Ile	Gly	Ile	Asn	Val
145							150			155				160	
Arg	Ala	Arg	Glu	Gly	Leu	Thr	Phe	Asp	Asn	Asp	Gly	Tyr	Leu	Val	Ala
165							170			175					
Trp	Asn	Pro	Lys	Tyr	Asp	Thr	Arg	Thr	Leu	Trp	Thr	Thr	Pro	Asp	Thr
180							185					190			
Ser	Pro	Asn	Cys	Thr	Ile	Ala	Gln	Asp	Lys	Asp	Ser	Lys	Leu	Thr	Leu
195							200			205					
Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Ile	Leu	Ala	Asn	Val	Ser	Leu	Ile
210							215			220					
Val	Val	Ala	Gly	Lys	Tyr	His	Ile	Ile	Asn	Asn	Lys	Thr	Asn	Pro	Glu
225							230			235				240	
Ile	Lys	Ser	Phe	Thr	Ile	Lys	Leu	Leu	Phe	Asn	Lys	Asn	Gly	Val	Leu
245							245			250				255	
Leu	Asp	Asn	Ser	Asn	Leu	Gly	Lys	Ala	Tyr	Trp	Asn	Phe	Arg	Ser	Gly
260							260			265				270	
Asn	Ser	Asn	Val	Ser	Thr	Ala	Tyr	Glu	Lys	Ala	Ile	Gly	Phe	Met	Pro
275							275			280				285	
Asn	Leu	Val	Ala	Tyr	Pro	Lys	Pro	Ser	Asn	Ser	Lys	Lys	Tyr	Ala	Arg
290							290			295				300	
Asp	Ile	Val	Tyr	Gly	Thr	Ile	Tyr	Leu	Gly	Gly	Lys	Pro	Asp	Gln	Pro
305							310			315				320	
Ala	Val	Ile	Lys	Thr	Thr	Phe	Asn	Gln	Glu	Thr	Gly	Cys	Glu	Tyr	Ser
325							325			330				335	
Ile	Thr	Phe	Asp	Phe	Ser	Trp	Ser	Lys	Thr	Tyr	Glu	Asn	Val	Glu	Phe
340							340			345				350	
Glu	Thr	Thr	Ser	Phe	Thr	Phe	Ser	Tyr	Ile	Ala	Gln	Glu			
355							355			360				365	

<210> 40  
<211> 1228

-28-

<212> DNA  
 <213> Adenovirus serotype 9 fiber  
 <220>  
 <221> CDS  
 <222> (50) ... (1138)

<400> 40  
 aaggatgtc aaattcctgg tccacaattt tcattgtctt ccctcttag atg tca aag 58  
 Met Ser Lys  
 1

agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc tat ggc tac	Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro Tyr Gly Tyr	106
5 10 15		
gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt gtc tcc tcc	Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser	154
20 25 30 35	20 25 30 35	
gat gga ttc caa aac ttc ccc cct ggg gtc ctg tca ctc aaa cta gct	Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala	202
40 45 50	40 45 50	
gac cca ata gcc atc gtc aat ggg aat gtc tca ctc aaa gtg gga ggg	Asp Pro Ile Ala Ile Val Asn Gly Asn Val Ser Leu Lys Val Gly Gly	250
55 60 65	55 60 65	
ggt ctc act ttg caa gat gga act gga aaa cta aca gtc aat gct gat	Gly Leu Thr Leu Gln Asp Gly Thr Gly Lys Leu Thr Val Asn Ala Asp	298
70 75 80	70 75 80	
cca cct ttg caa ctt aca aac aac aaa tta ggg att gct ttg gac gct	Pro Pro Leu Gln Leu Thr Asn Asn Lys Leu Gly Ile Ala Leu Asp Ala	346
85 90 95	85 90 95	
cca ttt gat gtt ata gat aat aaa ctc aca ttg tta gcg ggc cat ggc	Pro Phe Asp Val Ile Asp Asn Lys Leu Thr Leu Leu Ala Gly His Gly	394
100 105 110 115	100 105 110 115	
ttg tct att ata aca aaa gaa aca tca aca ctg cct ggc ttg agg aat	Leu Ser Ile Ile Thr Lys Glu Thr Ser Thr Leu Pro Gly Leu Arg Asn	442
120 125 130 135	120 125 130 135	
act ctt gta gta tta act gga aag ggt att gga aca gaa tca aca gat	Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu Ser Thr Asp	490
135 140 145	135 140 145	
aat ggc gga acg gta tgt gtt aga gtt gga gaa ggt ggc ggc tta tca	Asn Gly Gly Thr Val Cys Val Arg Val Gly Glu Gly Gly Leu Ser	538
150 155 160	150 155 160	
ttt aat aat gat gga gac ttg gta gca ttt aat aaa aaa gaa gat aag	Phe Asn Asn Asp Gly Asp Leu Val Ala Phe Asn Lys Lys Glu Asp Lys	586
165 170 175	165 170 175	
cgc acc cta tgg aca act cca gac aca tct cca aat tgc aag att gat	Arg Thr Leu Trp Thr Pro Asp Thr Ser Pro Asn Cys Lys Ile Asp	634
180 185 190 195	180 185 190 195	
cag gat aag gac tct aag tta act ctg gtc ctt aca aag tgt gga agt		682

-29-

Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser			
200	205	210	
caa ata ttg gct aat gtg tca tta att gtc gta gat ggt aag tac aaa			
Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Asp Gly Lys Tyr Lys			730
215	220	225	
att atc aat aac aat act caa cca gct ctc aaa gga ttt acc att aaa			
Ile Ile Asn Asn Asn Thr Gln Pro Ala Leu Lys Gly Phe Thr Ile Lys			778
230	235	240	
tta ttg ttt gat gaa aat gga gta ctt atg gaa tct tca aat ctt ggt			
Leu Leu Phe Asp Glu Asn Gly Val Leu Met Glu Ser Ser Asn Leu Gly			826
245	250	255	
aaa tca tat tgg aac ttt aga aat gaa aat tca att atg tca aca gct			
Lys Ser Tyr Trp Asn Phe Arg Asn Glu Asn Ser Ile Met Ser Thr Ala			874
260	265	270	275
tat gaa aaa gct att gga ttc atg cct aat ttg gta gcc tat cca aaa			
Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro Lys			922
280	285	290	
cct acc gct ggc tct aaa aaa tat gca aga gat ata gtt tat gga aac			
Pro Thr Ala Gly Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Asn			970
295	300	305	
atc tac ctt ggt gga aag cca gat caa cca gta acc att aaa act acc			
Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Val Thr Ile Lys Thr Thr			1018
310	315	320	
ttt aat cag gaa act gga tgt gaa tat tct atc aca ttt gat ttt agt			
Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asp Phe Ser			1066
325	330	335	
tgg gcc aag act tat gta aat gtt gaa ttt gaa aca acc tct ttt acc			
Trp Ala Lys Thr Tyr Val Asn Val Glu Phe Glu Thr Thr Ser Phe Thr			1114
340	345	350	355
ttt tcc tat atc gcc caa gaa tga aagaccaata aacgtgttt tcatttcaaa			1168
Phe Ser Tyr Ile Ala Gln Glu *			
360			
atttcatgt atcttattg attttacac cagcacgggt agtcagtctc ccaccaccag 1228			

<210> 41  
<211> 362

<212> PRT

<213> Adenovirus serotype 9 fiber

<400> 41

Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro			
1	5	10	15
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe			
20	25	30	
Val Ser Ser Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu			
35	40	45	
Lys Leu Ala Asp Pro Ile Ala Ile Val Asn Gly Asn Val Ser Leu Lys			
50	55	60	
Val Gly Gly Leu Thr Leu Gln Asp Gly Thr Gly Lys Leu Thr Val			

-30-

65	70	75	80
Asn Ala Asp Pro Pro Leu Gln Leu Thr Asn Asn Lys Leu Gly Ile Ala			
85	90	95	
Leu Asp Ala Pro Phe Asp Val Ile Asp Asn Lys Leu Thr Leu Leu Ala			
100	105	110	
Gly His Gly Leu Ser Ile Ile Thr Lys Glu Thr Ser Thr Leu Pro Gly			
115	120	125	
Leu Arg Asn Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu			
130	135	140	
Ser Thr Asp Asn Gly Gly Thr Val Cys Val Arg Val Gly Glu Gly Gly			
145	150	155	160
Gly Leu Ser Phe Asn Asn Asp Gly Asp Leu Val Ala Phe Asn Lys Lys			
165	170	175	
Glu Asp Lys Arg Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys			
180	185	190	
Lys Ile Asp Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys			
195	200	205	
Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Asp Gly			
210	215	220	
Lys Tyr Lys Ile Ile Asn Asn Asn Thr Gln Pro Ala Leu Lys Gly Phe			
225	230	235	240
Thr Ile Lys Leu Leu Phe Asp Glu Asn Gly Val Leu Met Glu Ser Ser			
245	250	255	
Asn Leu Gly Lys Ser Tyr Trp Asn Phe Arg Asn Glu Asn Ser Ile Met			
260	265	270	
Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala			
275	280	285	
Tyr Pro Lys Pro Thr Ala Gly Ser Lys Lys Tyr Ala Arg Asp Ile Val			
290	295	300	
Tyr Gly Asn Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Val Thr Ile			
305	310	315	320
Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe			
325	330	335	
Asp Phe Ser Trp Ala Lys Thr Tyr Val Asn Val Glu Phe Glu Thr Thr			
340	345	350	
Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu			
355	360		

&lt;210&gt; 42

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Ad2 third repeat

&lt;400&gt; 42

Gly Asn Leu Thr Ser Gln Asn Val Thr Thr Val Thr Gln Pro Leu Lys			
1	5	10	15
Lys Thr Lys Ser			
20			

&lt;210&gt; 43

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Ad5 third repeat

-31-

<400> 43  
Gly Asn Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys  
1 5 10 15  
Lys Thr Lys Ser 20

<210> 44  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Repeat motif

<221> VARIANT  
<222> 4  
<223> Xaa = Thr or Ser

<400> 44  
Thr Thr Val Xaa  
1

<210> 45  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Repeat Consensus Sequence

<221> VARIANT  
<222> 3,5,7,13  
<223> Xaa = Hydrophobic Amino Acid

<221> VARIANT  
<222> 1, 2, 4, 6, 8, 9, 11, 12, 14, 15  
<223> Xaa = Any Amino Acid

<221> VARIANT  
<222> 10  
<223> Xaa = Pro or Gly

<400> 45  
Xaa  
1 5 10 15

<210> 46  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Ad2 21st repeat

<400> 46  
Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp Asn Ser  
1 5 10 15

-32-

<210> 47  
<211> 16  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> Ad5 21st repeat  
  
<400> 47  
Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp Ser Thr  
1 5 10 15  
  
<210> 48  
<211> 16  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> Ad37 last repeat  
  
<400> 48  
Ile Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp  
1 5 10 15  
  
<210> 49  
<211> 9  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> Last repeat consensus sequence  
  
<221> VARIANT  
<222> 4, 7  
<223> Xaa = Any Amino Acid  
  
<221> VARIANT  
<222> 9  
<223> Xaa = Asp or Asn  
  
<400> 49  
Lys Leu Gly Xaa Gly Leu Xaa Phe Xaa  
1 5  
  
<210> 50  
<211> 1164  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Ad5Ds fiber  
  
<221> CDS  
<222> (13) ... (1092)  
  
<221> misc\_feature  
<222> 1130, 1157  
<223> n = A, T, C or G

-33-

<400> 50  
 atgggatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51  
           Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro  
           1                         5                         10  
  
 gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99  
 Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu  
           15                     20                         25  
  
 act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147  
 Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly  
           30                     35                         40                     45  
  
 gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg 195  
 Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met  
           50                     55                         60  
  
 ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac 243  
 Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn  
           65                     70                         75  
  
 ctt acc tcc caa aat gta acc act gtg agc cca cct ctc aaa aaa acc 291  
 Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr  
           80                     85                         90  
  
 aag aaa aag ctt gaa gtt aac cta agc act gcc aag ggg ttg atg ttt 339  
 Lys Lys Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe  
           95                     100                         105  
  
 gac gct aca gcc ata gcc att aat gca gga gat ggg ctt gaa ttt ggt 387  
 Asp Ala Thr Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly  
           110                     115                         120                     125  
  
 tca cct aat gca cca aac aca aat ccc ctc aaa aca aaa att ggc cat 435  
 Ser Pro Asn Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His  
           130                     135                         140  
  
 ggc cta gaa ttt gat tca aac aag gct atg gtt cct aaa cta gga act 483  
 Gly Leu Glu Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr  
           145                     150                         155  
  
 ggc ctt agt ttt gac agc aca ggt gcc att aca gta gga aac aaa aat 531  
 Gly Leu Ser Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn  
           160                     165                         170  
  
 aat gat aag cta act ttg tgg acc aca cca gct cca tct cct aac tgt 579  
 Asn Asp Lys Leu Thr Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys  
           175                     180                         185  
  
 aga cta aat gca gag aaa gat gct aaa ctc act ttg gtc tta aca aaa 627  
 Arg Leu Asn Ala Glu Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys  
           190                     195                         200                     205  
  
 tgt ggc agt caa ata ctt gct aca gtt tca gtt ttg gct gtt aaa ggc 675  
 Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly  
           210                     215                         220  
  
 agt ttg gct cca ata tct gga aca gtt caa agt gct cat ctt att ata 723  
 Ser Leu Ala Pro Ile Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile  
           225                     230                         235

-34-

aga ttt gac gaa aat gga gtg cta cta aac aat tcc ttc ctg gac cca	771
Arg Phe Asp Glu Asn Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro	
240 245 250	
gaa tat tgg aac ttt aga aat gga gat ctt act gaa ggc aca gcc tat	819
Glu Tyr Trp Asn Phe Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr	
255 260 265	
aca aac gct gtt gga ttt atg cct aac cta tca gct tat cca aaa tct	867
Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser	
270 275 280 285	
cac ggt aaa act gcc aaa agt aac att gtc agt caa gtt tac tta aac	915
His Gly Lys Thr Ala Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn	
290 295 300	
gga gac aaa act aaa cct gta aca cta acc att aca cta aac ggt aca	963
Gly Asp Lys Thr Lys Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr	
305 310 315	
cag gaa aca gga gac aca act cca agt gca tac tct atg tca ttt tca	1011
Gln Glu Thr Gly Asp Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser	
320 325 330	
tgg gac tgg tct ggc cac aac tac att aat gaa ata ttt gcc aca tcc	1059
Trp Asp Trp Ser Gly His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser	
335 340 345	
tct tac act ttt tca tac att gcc caa gaa taa agaagcggcc gcgttatgaa	1112
Ser Tyr Thr Phe Ser Tyr Ile Ala Gln Glu *	
350 355	
gggcgaattc cagcacantg gcggccgtta tttagtgatc cgagntcatg ca	1164
<210> 51	
<211> 359	
<212> PRT	
<213> Artificial Sequence	
<220>	
<223> Ad5deltas	
<400> 51	
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro	
1 5 10 15	
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro	
20 25 30	
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser	
35 40 45	
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu	
50 55 60	
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser	
65 70 75 80	
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Lys Lys	
85 90 95	
Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr	
100 105 110	
Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn	
115 120 125	
Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu	
130 135 140	

-35-

Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser  
 145 150 155 160  
 Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys  
 165 170 175  
 Leu Thr Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn  
 180 185 190  
 Ala Glu Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser  
 195 200 205  
 Gln Ile Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala  
 210 215 220  
 Pro Ile Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp  
 225 230 235 240  
 Glu Asn Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp  
 245 250 255  
 Asn Phe Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala  
 260 265 270  
 Val Gly Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys  
 275 280 285  
 Thr Ala Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys  
 290 295 300  
 Thr Lys Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr  
 305 310 315 320  
 Gly Asp Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp  
 325 330 335  
 Ser Gly His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr  
 340 345 350  
 Phe Ser Tyr Ile Ala Gln Glu  
 355

<210> 52  
<211> 1920  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Ad5s/Ad37k fiber

<221> CDS  
<222> (13)...(1755)

<221> misc\_feature  
<222> 1867, 1875  
<223> n = A,T,C or G

<400> 52  
gcaagatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51  
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro  
1 5 10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99  
Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu  
15 20 25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147  
Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly  
30 35 40 45

gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg 195  
Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met  
50 55 60

-36-

ctt	gct	ctc	aaa	atg	ggc	aac	ggc	ctc	tct	ctg	gac	gag	gcc	ggc	aac		243
Leu	Ala	Leu	Lys	Met	Gly	Asn	Gly	Leu	Ser	Leu	Asp	Glu	Ala	Gly	Asn		
				65				70				75					
ctt	acc	tcc	caa	aat	gtt	acc	act	gtt	agc	cca	cct	ctc	aaa	aaa	acc		291
Leu	Thr	Ser	Gln	Asn	Val	Thr	Thr	Val	Ser	Pro	Pro	Leu	Lys	Lys	Thr		
				80				85				90					
aag	tca	aac	ata	aac	ctg	gaa	ata	tct	gca	ccc	ctc	aca	gtt	acc	tca		339
Lys	Ser	Asn	Ile	Asn	Leu	Glu	Ile	Ser	Ala	Pro	Leu	Thr	Val	Thr	Ser		
				95				100				105					
gaa	gcc	cta	act	gtt	gct	gcc	gca	cct	cta	atg	gtc	gct	ggc	ggc	aac		387
Glu	Ala	Leu	Thr	Val	Ala	Ala	Ala	Ala	Pro	Leu	Met	Val	Ala	Gly	Asn		
				110				115			120			125			
aca	ctc	acc	atg	caa	tca	cag	gcc	ccg	cta	acc	gtt	cac	gac	tcc	aaa		435
Thr	Leu	Thr	Met	Gln	Ser	Gln	Ala	Pro	Leu	Thr	Val	His	Asp	Ser	Lys		
				130				135			140						
ctt	agc	att	gcc	acc	caa	gga	ccc	ctc	aca	gtt	tca	gaa	gga	aag	cta		483
Leu	Ser	Ile	Ala	Thr	Gln	Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu		
				145				150			155						
gcc	ctg	caa	aca	tca	ggc	ccc	ctc	acc	acc	acc	gat	agc	agt	acc	ctt		531
Ala	Leu	Gln	Thr	Ser	Gly	Pro	Leu	Thr	Thr	Asp	Ser	Ser	Ser	Thr	Leu		
				160				165			170						
act	atc	act	gcc	tca	ccc	cct	cta	act	act	gcc	act	ggt	agc	ttg	ggc		579
Thr	Ile	Thr	Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly		
				175				180			185						
att	gac	ttg	aaa	gag	ccc	att	tat	aca	caa	aat	gga	aaa	cta	gga	cta		627
Ile	Asp	Leu	Lys	Glu	Pro	Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu		
				190				195			200			205			
aag	tac	ggg	gct	cct	ttg	cat	gta	aca	gac	gac	cta	aac	act	ttg	acc		675
Lys	Tyr	Gly	Ala	Pro	Leu	His	Val	Thr	Asp	Asp	Leu	Asn	Thr	Leu	Thr		
				210				215			220						
gta	gca	act	ggt	cca	ggt	gtg	act	att	aat	aat	act	tcc	ttg	caa	act		723
Val	Ala	Thr	Gly	Pro	Gly	Val	Thr	Ile	Asn	Asn	Thr	Ser	Leu	Gln	Thr		
				225				230			235						
aaa	gtt	act	gga	gcc	ttg	ggt	ttt	gat	tca	caa	ggc	aat	atg	caa	ctt		771
Lys	Val	Thr	Gly	Ala	Leu	Gly	Phe	Asp	Ser	Gln	Gly	Asn	Met	Gln	Leu		
				240				245			250						
aat	gta	gca	gga	gga	cta	agg	att	gat	tct	caa	aac	aga	cgc	ctt	ata		819
Asn	Val	Ala	Gly	Gly	Leu	Arg	Ile	Asp	Ser	Gln	Asn	Arg	Arg	Leu	Ile		
				255				260			265						
ctt	gat	gtt	agt	tat	ccg	ttt	gat	gct	caa	aac	caa	cta	aat	cta	aga		867
Leu	Asp	Val	Ser	Tyr	Pro	Phe	Asp	Ala	Gln	Asn	Gln	Leu	Asn	Leu	Arg		
				270				275			280			285			
cta	gga	cag	ggc	cct	ttt	ata	aac	tca	gcc	cac	aac	ttg	gat	att		915	
Leu	Gly	Gln	Gly	Pro	Leu	Phe	Ile	Asn	Ser	Ala	His	Asn	Leu	Asp	Ile		
				290				295			300						

-37-

aac tac aac aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa Asn Tyr Asn Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys 305 310 315	963
aag ctt gag gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct Lys Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala 320 325 330	1011
aca gcc ata gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct Thr Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro 335 340 345	1059
aat gca cca aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta Asn Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu 350 355 360 365	1107
gaa ttt gat tca aac aag gct atg gtt cct aaa cta gga act ggc ctt Glu Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu 370 375 380	1155
agt ttt gac agc aca ggt gcc att aca gta gga aac aaa aat aat gat Ser Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp 385 390 395	1203
aag cta act ttg tgg acc aca cca gac act agt cca aac tgc aca att Lys Leu Thr Leu Trp Thr Pro Asp Thr Ser Pro Asn Cys Thr Ile 400 405 410	1251
gct caa gat aag gac tct aaa ctc act ttg gta ctt aca aag tgt gga Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly 415 420 425	1299
agt caa ata tta gct aat gtg tct ttg att gtg gtc gca gga aag tac Ser Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Ala Gly Lys Tyr 430 435 440 445	1347
cac atc ata aat aat aag aca aat cca aaa ata aaa agt ttt act att His Ile Asn Asn Lys Thr Asn Pro Lys Ile Lys Ser Phe Thr Ile 450 455 460	1395
aaa ctg cta ttt aat aag aac gga gtg ctt tta gac aac tca aat ctt Lys Leu Leu Phe Asn Lys Asn Gly Val Leu Leu Asp Asn Ser Asn Leu 465 470 475	1443
gga aaa gct tat tgg aac ttt aga agt gga aat tcc aat gtt tcg aca Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly Asn Ser Asn Val Ser Thr 480 485 490	1491
gct tat gaa aaa gca att ggt ttt atg cct aat ttg gta gcg tat cca Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro 495 500 505	1539
aaa ccc agt aat tct aaa aaa tat gca aga gac ata gtt tat gga act Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Thr 510 515 520 525	1587
ata tat ctt ggt gga aaa cct gat cag cca gca gtc att aaa act acc Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Ala Val Ile Lys Thr Thr 530 535 540	1635
ttt aac caa gaa act gga tgt gaa tac tct atc aca ttt aac ttt agt	1683

-38-

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Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asn Phe Ser
      545          550          555
tgg tcc aaa acc tat gaa aat gtt gaa ttt gaa acc acc tct ttt acc   1731
Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe Glu Thr Thr Ser Phe Thr
      560          565          570
ttc tcc tat att gcc caa gaa tga aaaagcggcc gctcgagtct agagggcccg  1785
Phe Ser Tyr Ile Ala Gln Glu *                               575
      580
tttaaacccg ctgatcagcc tcgactgtgc cttctagttg ccagccatct gttgtttgcc 1845
cctccccgt gccttccttg ancctggaa gtgccactcc cactgtcctt tcctaataaa 1905
atgaggaaat gcatac                                         1920

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<211> 580
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5s/Ad37k

<400> 53
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
  1           5           10          15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
  20          25          30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
  35          40          45
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
  50          55          60
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
  65          70          75          80
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
  85          90          95
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
 100         105         110
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
 115         120         125
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
 130         135         140
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
 145         150         155         160
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
 165         170         175
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
 180         185         190
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
 195         200         205
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
 210         215         220
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
 225         230         235         240
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
 245         250         255
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
 260         265         270
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
 275         280         285
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

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-39-

Lys	Gly	Leu	Tyr	Leu	Phe	Thr	Ala	Ser	Asn	Asn	Ser	Lys	Lys	Leu	Glu
290	295														
305	310														
Val	Asn	Leu	Ser	Thr	Ala	Lys	Gly	Leu	Met	Phe	Asp	Ala	Thr	Ala	Ile
Ala	Ile	Asn	Ala	Gly	Asp	Gly	Leu	Glu	Phe	Gly	Ser	Pro	Asn	Ala	Pro
Asn	Thr	Asn	Pro	Leu	Lys	Thr	Lys	Ile	Gly	His	Gly	Leu	Glu	Phe	Asp
Ser	Asn	Lys	Ala	Met	Val	Pro	Lys	Leu	Gly	Thr	Gly	Leu	Ser	Phe	Asp
Ser	Thr	Gly	Ala	Ile	Thr	Val	Gly	Asn	Lys	Asn	Asn	Asp	Lys	Leu	Thr
385	390														
Leu	Trp	Thr	Thr	Pro	Asp	Thr	Ser	Pro	Asn	Cys	Thr	Ile	Ala	Gln	Asp
Lys	Asp	Ser	Lys	Leu	Thr	Leu	Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Ile
420	425														
Leu	Ala	Asn	Val	Ser	Leu	Ile	Val	Val	Ala	Gly	Lys	Tyr	His	Ile	Ile
435	440														
Asn	Asn	Lys	Thr	Asn	Pro	Lys	Ile	Lys	Ser	Phe	Thr	Ile	Lys	Leu	Leu
450	455														
Phe	Asn	Lys	Asn	Gly	Val	Leu	Leu	Asp	Asn	Ser	Asn	Leu	Gly	Lys	Ala
465	470														
Tyr	Trp	Asn	Phe	Arg	Ser	Gly	Asn	Ser	Asn	Val	Ser	Thr	Ala	Tyr	Glu
485	490														
Lys	Ala	Ile	Gly	Phe	Met	Pro	Asn	Leu	Val	Ala	Tyr	Pro	Lys	Pro	Ser
500	505														
Asn	Ser	Lys	Lys	Tyr	Ala	Arg	Asp	Ile	Val	Tyr	Gly	Thr	Ile	Tyr	Leu
515	520														
Gly	Gly	Lys	Pro	Asp	Gln	Pro	Ala	Val	Ile	Lys	Thr	Thr	Phe	Asn	Gln
530	535														
Glu	Thr	Gly	Cys	Glu	Tyr	Ser	Ile	Thr	Phe	Asn	Phe	Ser	Trp	Ser	Lys
545	550														
Thr	Tyr	Glu	Asn	Val	Glu	Phe	Glu	Thr	Thr	Ser	Phe	Thr	Phe	Ser	Tyr
555	565														
Ile	Ala	Gln	Glu												
580															

<210> 54  
<211> 1767  
<212> DNA  
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<220>  
<223> Ad5s/Ad37s fiber

<221> CDS  
<222> (13)...(1749)

<400> 54

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      Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
          1           5           10
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gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99
Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
    15          20          25
```

```
act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147
Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
```

-40-

30	35	40	45	
gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met				195
50	55	60		
ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc agc Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Ser				243
65	70	75		
cta act gta aac cct aag gct cca ctg caa gtt aat act gat tca aac Leu Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Ser Asn				291
80	85	90		
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu				339
95	100	105		
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr				387
110	115	120	125	
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile				435
130	135	140		
gcc acc caa gga ccc ctc aca acc acc gat agc agt acc ctt act atc act Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln				483
145	150	155		
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr				531
160	165	170		
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu				579
175	180	185		
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly				627
190	195	200	205	
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr				675
210	215	220		
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr				723
225	230	235		
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala				771
240	245	250		
gga gga cta agg att gat tct caa aac aca aga cgc ctt ata ctt gat gtt Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val				819
255	260	265		
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln				867
270	275	280	285	

-41-

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac	915
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn	
290 295 300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag	963
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu	
305 310 315	
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata	1011
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile	
320 325 330	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca	1059
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro	
335 340 345	
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat	1107
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp	
350 355 360 365	
tca aac att ggt ata aat gta aga gca aga gaa ggg ttg aca ttt gac	1155
Ser Asn Ile Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp	
370 375 380	
aat gat ggt gcc att aca gta gga aac aaa aat aat gat aag cta act	1203
Asn Asp Gly Ala Ile Thr Val Gly Asn Lys Asn Asp Lys Leu Thr	
385 390 395	
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag	1251
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu	
400 405 410	
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata	1299
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile	
415 420 425	
ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata	1347
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile	
430 435 440 445	
tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat	1395
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn	
450 455 460	
gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt	1443
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe	
465 470 475	
aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga	1491
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly	
480 485 490	
ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc	1539
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala	
495 500 505	
aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa	1587
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys	
510 515 520 525	

-42-

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac	1635
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp	
530 535 540	
aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc	1683
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly	
545 550 555	
cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca	1731
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser	
560 565 570	
tac att gcc caa gaa taa agaagcggcc gcgttatg	1767
Tyr Ile Ala Gln Glu *	
575	

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<211> 578  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Ad5s/Ad37s

<400> 55	
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro	
1 5 10 15	
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro	
20 25 30	
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser	
35 40 45	
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu	
50 55 60	
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Ser Leu Thr Val	
65 70 75 80	
Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Ser Asn Ile Asn Leu	
85 90 95	
Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu Thr Val Ala	
100 105 110	
Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr Met Gln Ser	
115 120 125	
Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile Ala Thr Gln	
130 135 140	
Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln Thr Ser Gly	
145 150 155 160	
Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr Ala Ser Pro	
165 170 175	
Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu Lys Glu Pro	
180 185 190	
Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly Ala Pro Leu	
195 200 205	
His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr Gly Pro Gly	
210 215 220	
Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr Gly Ala Leu	
225 230 235 240	
Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala Gly Gly Leu	
245 250 255	
Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val Ser Tyr Pro	
260 265 270	
Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln Gly Pro Leu	

-43-

Phe	Ile	Asn	Ser	Ala	His	Asn	Leu	Asp	Ile	Asn	Tyr	Asn	Lys	Gly	Leu
275							280					285			
290							295					300			
Tyr	Leu	Phe	Thr	Ala	Ser	Asn	Asn	Ser	Lys	Lys	Leu	Glu	Val	Asn	Leu
305							310					315			320
Ser	Thr	Ala	Lys	Gly	Leu	Met	Phe	Asp	Ala	Thr	Ala	Ile	Ala	Ile	Asn
						325					330			335	
Ala	Gly	Asp	Gly	Leu	Glu	Phe	Gly	Ser	Pro	Asn	Ala	Pro	Asn	Thr	Asn
						340					345			350	
Pro	Leu	Lys	Thr	Lys	Ile	Gly	His	Gly	Leu	Glu	Phe	Asp	Ser	Asn	Ile
						355					360			365	
Gly	Ile	Asn	Val	Arg	Ala	Arg	Glu	Gly	Leu	Thr	Phe	Asp	Asn	Asp	Gly
						370					375			380	
Ala	Ile	Thr	Val	Gly	Asn	Asn	Asp	Lys	Leu	Thr	Leu	Trp	Thr		
						385					390			395	
Thr	Pro	Ala	Pro	Ser	Pro	Asn	Cys	Arg	Leu	Asn	Ala	Glu	Lys	Asp	Ala
						405					410			415	
Lys	Leu	Thr	Leu	Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Ile	Leu	Ala	Thr
						420					425			430	
Val	Ser	Val	Leu	Ala	Val	Lys	Gly	Ser	Leu	Ala	Pro	Ile	Ser	Gly	Thr
						435					440			445	
Val	Gln	Ser	Ala	His	Leu	Ile	Ile	Arg	Phe	Asp	Glu	Asn	Gly	Val	Leu
						450					455			460	
Leu	Asn	Asn	Ser	Phe	Leu	Asp	Pro	Glu	Tyr	Trp	Asn	Phe	Arg	Asn	Gly
						465					470			475	
Asp	Leu	Thr	Glu	Gly	Thr	Ala	Tyr	Thr	Asn	Ala	Val	Gly	Phe	Met	Pro
						485					490			495	
Asn	Leu	Ser	Ala	Tyr	Pro	Lys	Ser	His	Gly	Lys	Thr	Ala	Lys	Ser	Asn
						500					505			510	
Ile	Val	Ser	Gln	Val	Tyr	Leu	Asn	Gly	Asp	Lys	Thr	Lys	Pro	Val	Thr
						515					520			525	
Leu	Thr	Ile	Thr	Leu	Asn	Gly	Thr	Gln	Glu	Thr	Gly	Asp	Thr	Thr	Pro
						530					535			540	
Ser	Ala	Tyr	Ser	Met	Ser	Phe	Ser	Trp	Asp	Trp	Ser	Gly	His	Asn	Tyr
						545					550			555	
Ile	Asn	Glu	Ile	Phe	Ala	Thr	Ser	Ser	Tyr	Thr	Phe	Ser	Tyr	Ile	Ala
						565					570			575	
Gln	Glu														

<210> 56

<211> 1132

<212> DNA

<213> Artificial Sequence

<220>

<223> Ad37s/Ad5k fiber

<221> CDS

<222> (16)...(1116)

<221> misc\_feature

<222> 1125

<223> n = A,T,C or G

<400> 56

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                   Met Lys Arg Ala Arg Pro Ser Glu Asp Asp Phe Asn  
                   1               5                                   10

-44-

ccc gtc tac ccc tat ggc tac gcg cg <sub>g</sub> aat cag aat atc ccc ttc ctc	99
Pro Val Tyr Pro Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu	
15 20 25	
act ccc ccc ttt gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg	147
Thr Pro Pro Phe Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly	
30 35 40	
gta ctg tca ctc aaa ctg gct gat cca atc acc att acc aat ggg gat	195
Val Leu Ser Leu Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp	
45 50 55 60	
gta tcc ctc aag gtg gga ggt ggt ctc act ttg caa gat gga agc cta	243
Val Ser Leu Lys Val Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu	
65 70 75	
act gta aac cct aag gct cca ctg caa gtt aat act gat aaa aaa ctt	291
Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu	
80 85 90	
gag ctt gca tat gat aat cca ttt gaa agt agt gct aat aaa ctt agt	339
Glu Leu Ala Tyr Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser	
95 100 105	
tta aaa gta gga cat gga tta aaa gta tta gat gaa aaa agt gct gcg	387
Leu Lys Val Gly His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala	
110 115 120	
ggg tta aaa gat tta att ggc aaa ctt gtg gtt tta aca gga aaa gga	435
Gly Leu Lys Asp Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly	
125 130 135 140	
ata ggc act gaa aat tta gaa aat aca gat ggt agc agc aga gga att	483
Ile Gly Thr Glu Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile	
145 150 155	
ggt ata aat gta aga gca aga gaa ggg ttg aca ttt gac aat gat gga	531
Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly	
160 165 170	
tac ttg gta gca tgg aac cca aag tat gac acg cgc act ttg tgg acc	579
Tyr Leu Val Ala Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr	
175 180 185	
aca cca gct cca tct cct aac tgg aga cta aat gca gag aaa gat gct	627
Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala	
190 195 200	
aaa ctc act ttg gtc tta aca aaa tgg ggc agt caa ata ctt gct aca	675
Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr	
205 210 215 220	
gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata tct gga aca	723
Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr	
225 230 235	
gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga gtg cta	771
Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu	
240 245 250	
cta aac aat tcc ttc ctg gat cca gaa tat tgg aac ttt aga aat gga	819

-45-

Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly				
255	260	265		
gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt atg cct			867	
Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro	270	275	280	
aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa agt aac			915	
Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn	285	290	295	300
att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta aca			963	
Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr	305	310	315	
ctt acc att aca cta aac ggt aca cag gaa aca gga gac aca act cca			1011	
Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro	320	325	330	
agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac tac			1059	
Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr	335	340	345	
att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att gcc			1107	
Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile Ala	350	355	360	
caa gaa taa agaagcggnc gctcga			1132	
Gln Glu *				
365				

<210> 57  
<211> 366  
<212> PRT  
<213> Artificial Sequence

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<223> Ad37s/Ad5k

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Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu  
35 40 45  
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys  
50 55 60  
Val Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro  
65 70 75 80  
Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr  
85 90 95  
Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly  
100 105 110  
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp  
115 120 125  
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu  
130 135 140  
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val  
145 150 155 160

-46-

Arg	Ala	Arg	Glu	Gly	Leu	Thr	Phe	Asp	Asn	Asp	Gly	Tyr	Leu	Val	Ala
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Trp	Asn	Pro	Lys	Tyr	Asp	Thr	Arg	Thr	Leu	Trp	Thr	Thr	Pro	Ala	Pro
				180				185					190		
Ser	Pro	Asn	Cys	Arg	Leu	Asn	Ala	Glu	Lys	Asp	Ala	Lys	Leu	Thr	Leu
				195				200				205			
Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Ile	Leu	Ala	Thr	Val	Ser	Val	Leu
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Ala	Val	Lys	Gly	Ser	Leu	Ala	Pro	Ile	Ser	Gly	Thr	Val	Gln	Ser	Ala
	225				230				235			240			
His	Leu	Ile	Ile	Arg	Phe	Asp	Glu	Asn	Gly	Val	Leu	Leu	Asn	Asn	Ser
				245					250			255			
Phe	Leu	Asp	Pro	Glu	Tyr	Trp	Asn	Phe	Arg	Asn	Gly	Asp	Leu	Thr	Glu
				260				265			270				
Gly	Thr	Ala	Tyr	Thr	Asn	Ala	Val	Gly	Phe	Met	Pro	Asn	Leu	Ser	Ala
	275				280				285			290			
Tyr	Pro	Lys	Ser	His	Gly	Lys	Thr	Ala	Lys	Ser	Asn	Ile	Val	Ser	Gln
	290				295				300			305			
Val	Tyr	Leu	Asn	Gly	Asp	Lys	Thr	Lys	Pro	Val	Thr	Leu	Thr	Ile	Thr
	305				310				315			320			
Leu	Asn	Gly	Thr	Gln	Glu	Thr	Gly	Asp	Thr	Thr	Pro	Ser	Ala	Tyr	Ser
				325				330			335				
Met	Ser	Phe	Ser	Trp	Asp	Trp	Ser	Gly	His	Asn	Tyr	Ile	Asn	Glu	Ile
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Phe	Ala	Thr	Ser	Ser	Tyr	Thr	Phe	Ser	Tyr	Ile	Ala	Gln	Glu		
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<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Ad37 third repeat

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<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Ad8 last repeat

<400> 59

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<210> 60

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<212> PRT

<213> Artificial Sequence

<220>

<223> Ad9 last repeat

-47-

<400> 60  
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<212> PRT  
<213> Artificial Sequence

<220>  
<223> Ad15 last repeat

<400> 61  
Val Arg Val Gly Glu Gly Gly Gly Leu Ser Phe Asn Glu Ala  
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<210> 62  
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<213> Artificial Sequence

<220>  
<223> Penton region

<400> 62  
His Ala Ile Arg Gly Asp Thr Phe  
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<210> 63  
<211> 15  
<212> PRT  
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<220>  
<223> Penton amino acid replacement

<400> 63  
Ser Arg Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Ser  
1 5 10 15

<210> 64  
<211> 4  
<212> PRT  
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<220>  
<223> Fiber protein conserved sequence

<400> 64  
Thr Trp Leu Thr  
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<210> 65  
<211> 4  
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<213> Artificial Sequence

-48-

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<220>
<223> HSP binding motif

<400> 65
Lys Lys Thr Lys
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<210> 66
<211> 16
<212> PRT
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<220>
<223> Ad8 third repeat

<400> 66
Gly Lys Leu Thr Val Asn Thr Glu Pro Pro Leu His Leu Thr Asn Asn
 1           5           10          15

<210> 67
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad9 third repeat

<400> 67
Gly Lys Leu Thr Val Asn Ala Asp Pro Pro Leu Gln Leu Thr Asn Asn
 1           5           10          15

<210> 68
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad15 third repeat

<400> 68
Gly Asn Leu Thr Val Asn Thr Glu Pro Pro Leu Gln Leu Thr Asn Asn
 1           5           10          15

<210> 69
<211> 3929
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector pCR2.1

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ttgtgagcgg ataacaattt cacacaggaa acagctatga ccatgattac gccaagcttg 240
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-49-

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-50-

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<212> DNA
<213> Artificial Sequence

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<223> Vector pCR2.1-Topo

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-51-

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